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OM protein - protein search, using sw model

Run on: February 9, 2006, 13:09:16 ; Search time 50 Seconds
(without alignments)
9.921 Million cell updates/sec

Title: US-10-705-857-2

Perfect score: 30

Sequence: 1 BEMQR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	30	100.0	106	2	US-09-513-999C-7907 Sequence 7907, Ap
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6	30	100.0	206	1	US-08-393-985-18 Sequence 18, Appl
7	30	100.0	206	2	US-08-819-286-1 Sequence 1, Appl
8	30	100.0	206	2	US-09-949-016-6311 Sequence 6311, Ap
9	30	100.0	219	2	US-09-949-016-10671 Sequence 10671, A
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11	27	90.0	200	2	US-09-252-991A-23347 Sequence 23347, A
12	27	90.0	215	2	US-09-248-796A-19812 Sequence 19812, A
13	27	90.0	231	2	US-09-252-991A-27366 Sequence 27366, A
14	27	90.0	231	2	US-09-502-540-13879 Sequence 13879, A
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17	27	90.0	375	1	US-07-803-6228-9 Sequence 9, Appl
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21	27	90.0	727	2	US-09-487-558B-296 Sequence 296, Ap
22	27	90.0	729	2	US-07-803-6228-2 Sequence 2, Appl
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34	27	90.0	2133	1	US-09-037-601-37 Sequence 37, Appl
35	27	90.0	2133	2	US-09-315-179-37 Sequence 37, Appl
36	27	90.0	2133	2	US-09-523-656-30 Sequence 30, Appl
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95	25	83.3	753	2	US-10-147-928-6 Sequence 6, Appl
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OM protein - protein search, using SW model

Run on: February 9, 2006, 13:13:17 ; Search time 63 Seconds
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39.793 Million cell updates/sec

Title: US-10-705-857-2

Sequence: 1 BEMQR 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database : Published Applications AA Main:*

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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	30	100.0	13	4	US-10-705-857-3
3	30	100.0	82	4	US-10-705-857-1
4	30	100.0	93	4	US-10-282-122A-71377
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15	30	100.0	206	5	US-10-723-860-1223
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18	30	100.0	206	5	US-10-917-844-90
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31	27	90.0	86	5	US-10-499-065A-507	Sequence 507, App
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33	27	90.0	101	4	US-10-437-963-179345	Sequence 179345,
34	27	90.0	149	4	US-10-424-599-208350	Sequence 208350,
35	27	90.0	164	4	US-10-425-115-341520	Sequence 341520,
36	27	90.0	180	4	US-10-424-599-186497	Sequence 186497,
37	27	90.0	185	4	US-10-437-963-144759	Sequence 144759,
38	27	90.0	205	4	US-10-424-599-237624	Sequence 237624,
39	27	90.0	210	4	US-10-437-963-141286	Sequence 141286,
40	27	90.0	213	4	US-10-767-701-43626	Sequence 43626, A
41	27	90.0	214	3	US-09-925-300-1287	Sequence 1287, Ap
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46	27	90.0	245	3	US-09-925-299-791	Sequence 791, App
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77	27	90.0	516	4	US-10-425-114-40229	Sequence 40229, A
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134	27	90.0	2114	4	US-10-721-997A-33	Sequence 33, App1	207	26	86.7	493	4	US-10-282-122A-69984	Sequence 69984, A
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143	26	86.7	73	4	US-10-437-963-116997	Sequence 116997, A	216	26	86.7	621	5	US-10-370-715B-30	Sequence 30, App1
144	26	86.7	81	4	US-10-425-115-218608	Sequence 218608, A	217	26	86.7	635	4	US-10-437-963-194379	Sequence 194379, A
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146	26	86.7	90	4	US-10-767-701-60907	Sequence 60907, A	219	26	86.7	640	4	US-10-425-115-348561	Sequence 348561, A
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148	26	86.7	100	4	US-10-425-115-304647	Sequence 304647, A	221	26	86.7	663	3	US-09-925-298-654	Sequence 654, App
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151	26	86.7	111	4	US-10-767-701-43191	Sequence 43191, A	224	26	86.7	672	4	US-10-094-749-1885	Sequence 1885, Ap
152	26	86.7	112	4	US-10-425-115-368452	Sequence 368452, A	225	26	86.7	694	4	US-10-057-475B-10969	Sequence 10969, A
153	26	86.7	120	3	US-09-809-920-6	Sequence 6, App1	226	26	86.7	694	4	US-10-154-886B-10969	Sequence 10969, A
154	26	86.7	126	4	US-10-424-599-155414	Sequence 155414, A	227	26	86.7	709	4	US-10-425-115-348560	Sequence 348560, A
155	26	86.7	129	4	US-10-425-115-307676	Sequence 307676, A	228	26	86.7	715	4	US-10-425-114-38561	Sequence 38561, A
156	26	86.7	132	4	US-10-425-115-255019	Sequence 255019, A	229	26	86.7	718	4	US-10-142-143-20	Sequence 20, App1
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168	26	86.7	265	4	US-10-425-115-307674	Sequence 307674, A	241	26	86.7	956	4	US-10-108-260A-1037	Sequence 3037, Ap
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170	26	86.7	267	4	US-10-424-599-284438	Sequence 284438, A	243	26	86.7	962	5	US-10-733-923-22453	Sequence 22453, A
171	26	86.7	270	4	US-10-467-701-51620	Sequence 51620, A	244	26	86.7	970	6	US-11-097-143-2664	Sequence 2664, Ap
172	26	86.7	279	4	US-10-424-599-195189	Sequence 195189, A	245	26	86.7	1016	4	US-10-425-115-333729	Sequence 333729, A
173	26	86.7	305	4	US-10-128-714-3145	Sequence 3145, Ap	246	26	86.7	1057	4	US-10-425-115-275370	Sequence 275370, A

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OM protein - protein search, using sw model

Run on: February 9, 2006, 13:13:31 / Search time 8 Seconds
(without alignments)
9.842 Million cell updates/sec

Title: US-10-705-857-2

Perfect score: 30
Sequence: 1 BEMORR 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	206	7	US-11-169-041-225 Sequence 225, App
2	27	90.0	101	7	US-11-182-016-47 Sequence 47, App1
3	27	90.0	841	7	US-11-098-686-10188 Sequence 10188, A
4	26	86.7	829	6	US-10-821-234-1179 Sequence 1179, Ap
5	25	83.3	241	7	US-11-152-366-279 Sequence 279, App
6	25	83.3	265	7	US-11-098-686-10694 Sequence 10694, A
7	25	83.3	290	6	US-10-467-657-5128 Sequence 5128, Ap
8	25	83.3	323	7	US-11-156-084-300 Sequence 300, App
9	25	83.3	359	7	US-11-152-366-38 Sequence 38, App1
10	25	83.3	390	7	US-11-129-143-178 Sequence 178, App
11	25	83.3	461	6	US-10-878-556A-162 Sequence 162, App
12	25	83.3	469	6	US-10-821-234-1151 Sequence 1151, Ap
13	25	83.3	470	6	US-10-878-556A-101 Sequence 101, App
14	25	83.3	558	6	US-10-467-657-4258 Sequence 4258, Ap
15	25	83.3	770	7	US-11-070-627-8 Sequence 8, App1
16	25	83.3	770	7	US-11-070-627-10 Sequence 10, App1
17	25	83.3	1260	7	US-11-241-056-14 Sequence 14, App1
18	24	80.0	180	6	US-10-821-234-1689 Sequence 1689, Ap
19	24	80.0	320	6	US-10-689-742-84 Sequence 84, App1
20	24	80.0	320	6	US-10-793-626-1786 Sequence 1786, Ap
21	24	80.0	397	6	US-10-467-657-3814 Sequence 3814, Ap
22	24	80.0	528	6	US-10-511-538-255 Sequence 255, App
23	24	80.0	592	7	US-11-059-292A-10 Sequence 10, App1
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31	23	76.7	10	7	US-11-141-725-51 Sequence 51, App1
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33	23	76.7	138	6	US-11-124-368A-229 Sequence 229, App
34	23	76.7	148	6	US-10-530-253-22 Sequence 22, App1
35	23	76.7	178	7	US-11-124-368A-230 Sequence 230, App1
36	23	76.7	227	7	US-11-124-368A-231 Sequence 231, App
37	23	76.7	272	6	US-10-793-626-588 Sequence 588, App
38	23	76.7	302	7	US-11-156-084-355 Sequence 355, App
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49	23	76.7	413	6	US-10-967-648A-8 Sequence 8, App1
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52	23	76.7	508	6	US-10-878-556A-154 Sequence 154, App
53	23	76.7	531	7	US-11-060-914-4 Sequence 4, App1
54	23	76.7	611	7	US-11-010-239-129 Sequence 129, App
55	23	76.7	687	6	US-10-714-887-268 Sequence 268, App
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69	23	76.7	2084	6	US-10-055-877-73 Sequence 73, App1
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129	22	73.3	601	6	US-10-821-234-958	Sequence 110, App
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147	22	73.3	834	6	US-10-928-446A-200	Sequence 202, App
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166	22	73.3	2036	7	US-11-124-368A-281	Sequence 467, App
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168	22	73.3	2144	7	US-11-124-368A-277	Sequence 363, App
169	22	73.3	2531	7	US-11-124-367A-467	Sequence 363, App
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OM protein - protein search, using sw model

Run on: February 9, 2006, 13:25:17, Search time 599 Seconds
(without alignments)
13.843 Million cell updates/sec

Title: us-10-705-857-2

Perfect score: 30

Sequence: 1 BEMQRR 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database: Pending Patents_AA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Fri Feb 10 09:12:21 2006

us-10-

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 9, 2006, 13:25:37, Search time 34 Seconds
(without alignments)
12.433 Million cell updates/sec

Title: us-10-705-857-2

Perfect score: 30

Sequence: 1 BEMQRR 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 267388 seqs, 70454031 residues

Total number of hits satisfying chosen parameters: 267388

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

Database: Pending Patents_AA_New:*

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5: /cgn2_6/ptodata/2/paa/US08 NEW COMB.pep:*
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8: /cgn2_6/ptodata/2/paa/US10 NEW COMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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